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OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/046,433

DATE: 01/28/2002
TIME: 13:44:34

Input Set : A:\PF511P1 seqlisting.txt
Output Set: N:\CRF3\01282002\J046433.raw

C--> 3 <110> APPLICANT: Human Genome Sciences, Inc.
5 <120> TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR13 and TR14
7 <130> FILE REFERENCE: PF511P1
9 <140> CURRENT APPLICATION NUMBER: US/10/046,433

10 <141> CURRENT FILING DATE: 2002-01-16
12 <150> PRIOR APPLICATION NUMBER: 60/261,960
13 <151> PRIOR FILING DATE: 2001-01-17
15 <150> PRIOR APPLICATION NUMBER: 09/618,570
16 <151> PRIOR FILING DATE: 2000-07-14
18 <150> PRIOR APPLICATION NUMBER: 60/144,087
19 <151> PRIOR FILING DATE: 1999-07-16
21 <150> PRIOR APPLICATION NUMBER: 60/149,450
22 <151> PRIOR FILING DATE: 1999-07-18
24 <150> PRIOR APPLICATION NUMBER: 60/149,712
25 <151> PRIOR FILING DATE: 1999-08-20
27 <150> PRIOR APPLICATION NUMBER: 60/153,089
28 <151> PRIOR FILING DATE: 1999-09-10
30 <160> NUMBER OF SEQ ID NOS: 61
32 <170> SOFTWARE: PatentIn Ver. 2.0
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 2554
36 <212> TYPE: DNA
37 <213> ORGANISM: Homo sapiens
39 <220> FEATURE:
40 <221> NAME/KEY: CDS
41 <222> LOCATION: (31)..(2283)
43 <400> SEQUENCE: 1

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45 1 5
46
48 gct ggt gag aaa cat tgc cat aac agg ggt ggc cta cac ttc aga atg 102
Ala Gly Glu Lys His Cys His Asn Arg Gly Gly Leu His Phe Arg Met
50 10 15 20
52 ctt ccc ctg caa acc tgg cac gta tgc aga caa gca ggg ctg ctc ttt 150
Leu Pro Leu Gln Thr Trp His Val Cys Arg Gln Ala Gly Leu Leu Phe
54 25 30 35 40
56 ctg caa act ttg ccc agc aac tct tat tca aat aaa gga gaa act tct 198
Leu Gln Thr Leu Pro Ser Asn Ser Tyr Ser Asn Lys Gly Glu Thr Ser
58 45 50 55
60 tgc cac cag tgt gac cct gac aaa tac tca gag aaa gga tct tct tcc 246
Cys His Gln Cys Asp Pro Asp Lys Tyr Ser Glu Lys Gly Ser Ser Ser
62 60 65 70
64 tgt aac gtg cgc cca gct tgc aca gac aaa gat tat ttc tac aca cac 294

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65 Cys Asn Val Arg Pro Ala Cys Thr Asp Lys Asp Tyr Phe Tyr Thr His
66          75          80          85
68 acg gcc tgc gat gcc aac gga gag aca caa ctc atg tac aaa tgg gcc 342
69 Thr Ala Cys Asp Ala Asn Gly Glu Thr Gln Leu Met Tyr Lys Trp Ala
70          90          95          100
72 aag ccg aaa atc tgt agc gag gac ctt gag ggg gca gtg aag ctg cct 390
73 Lys Pro Lys Ile Cys Ser Glu Asp Leu Glu Gly Ala Val Lys Leu Pro
74 105          110          115          120
76 gcc tct ggt gtg aag acc cac tgc cca ccc tgc aac cca ggc ttc ttc 438
77 Ala Ser Gly Val Lys Thr His Cys Pro Pro Cys Asn Pro Gly Phe Phe
78          125          130          135
80 aaa acc aac aac agc acc tgc cag ccc tgc cca tat ggt tcc tac tcc 486
81 Lys Thr Asn Asn Ser Thr Cys Gln Pro Cys Pro Tyr Gly Ser Tyr Ser
82          140          145          150
84 aat ggc tca gac tgt acc cgc tgc cct gca ggg act gaa cct gct gtg 534
85 Asn Gly Ser Asp Cys Thr Arg Cys Pro Ala Gly Thr Glu Pro Ala Val
86          155          160          165
88 gga ttt gaa tac aaa tgg tgg aac acg ctg ccc aca aac atg gaa acg 582
89 Gly Phe Glu Tyr Lys Trp Trp Asn Thr Leu Pro Thr Asn Met Glu Thr
90          170          175          180
92 acc gtt ctc agt ggg atc aac ttc gag tac aag ggc atg aca ggc tgg 630
93 Thr Val Leu Ser Gly Ile Asn Phe Glu Tyr Lys Gly Met Thr Gly Trp
94 185          190          195          200
96 gag gtg gct ggt gat cac att tac aca gct gct gga gcc tca gac aat 678
97 Glu Val Ala Gly Asp His Ile Tyr Thr Ala Ala Gly Ala Ser Asp Asn
98          205          210          215
100 gac ttc atg att ctc act ctg gtt gtg cca gga ttt aga cct ccg cag 726
101 Asp Phe Met Ile Leu Thr Leu Val Val Pro Gly Phe Arg Pro Pro Gln
102          220          225          230
104 tcg gtg atg gca gac aca gag aat aaa gag gtg gcc aga atc aca ttt 774
105 Ser Val Met Ala Asp Thr Glu Asn Lys Glu Val Ala Arg Ile Thr Phe
106          235          240          245
108 gtc ttt gag acc ctc tgt tct gtg aac tgt gag ctc tac ttc atg gtg 822
109 Val Phe Glu Thr Leu Cys Ser Val Asn Cys Glu Leu Tyr Phe Met Val
110          250          255          260
112 ggt gtg aat tct agg acc aac act cct gtg gag acg tgg aaa ggt tcc 870
113 Gly Val Asn Ser Arg Thr Asn Thr Pro Val Glu Thr Trp Lys Gly Ser
114 265          270          275          280
116 aaa ggc aaa cag tcc tat acc tac atc att gag gag aac act acc acg 918
117 Lys Gly Lys Gln Ser Tyr Thr Tyr Ile Ile Glu Glu Asn Thr Thr Thr
118          285          290          295
120 agc ttc acc tgg gcc ttc cag agg acc act ttt cat gag gca agc agg 966
121 Ser Phe Thr Trp Ala Phe Gln Arg Thr Thr Phe His Glu Ala Ser Arg
122          300          305          310
124 aag tac acc aat gac gtt gcc aag atc tac tcc atc aat gtc acc aat 1014
125 Lys Tyr Thr Asn Asp Val Ala Lys Ile Tyr Ser Ile Asn Val Thr Asn
126          315          320          325
128 gtt atg aat ggc gtg gcc tcc tac tgc cgt ccc tgt gcc cta gaa gcc 1062
129 Val Met Asn Gly Val Ala Ser Tyr Cys Arg Pro Cys Ala Leu Glu Ala

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130	330	335	340		
132	tct gat gtg ggc tcc tcc tgc acc tct tgt cct gct ggt tac tat att	1110			
133	Ser Asp Val Gly Ser Ser Cys Thr Ser Cys Pro Ala Gly Tyr Tyr Ile				
134	345	350	355	360	
136	gac cga gat tca gga acc tgc cac tcc tgc ccc cct aac aca att ctg	1158			
137	Asp Arg Asp Ser Gly Thr Cys His Ser Cys Pro Pro Asn Thr Ile Leu				
138	365	370	375		
140	aaa gcc cac cag cct tat ggt gtc cag gcc tgt gtg ccc tgt ggt cca	1206			
141	Lys Ala His Gln Pro Tyr Gly Val Gln Ala Cys Val Pro Cys Gly Pro				
142	380	385	390		
144	ggg acc aag aac aac aag atc cac tct ctg tgc tac aat gat tgc acc	1254			
145	Gly Thr Lys Asn Asn Lys Ile His Ser Leu Cys Tyr Asn Asp Cys Thr				
146	395	400	405		
148	ttc tca cgc aac act cca acc agg act ttc aac tac aac ttc tcc gct	1302			
149	Phe Ser Arg Asn Thr Pro Thr Arg Thr Phe Asn Tyr Asn Phe Ser Ala				
150	410	415	420		
152	ttg gca aac acc gtc act ctt gct gga ggg cca agc ttc act tcc aaa	1350			
153	Leu Ala Asn Thr Val Thr Leu Ala Gly Gly Pro Ser Phe Thr Ser Lys				
154	425	430	435	440	
156	ggg ttg aaa tac ttc cat cac ttt acc ctc agt ctc tgt gga aac cag	1398			
157	Gly Leu Lys Tyr Phe His His Phe Thr Leu Ser Leu Cys Gly Asn Gln				
158	445	450	455		
160	ggt agg aaa atg tct gtg tgc acc gac aat gtc act gac ctc cgg att	1446			
161	Gly Arg Lys Met Ser Val Cys Thr Asp Asn Val Thr Asp Leu Arg Ile				
162	460	465	470		
164	cct gag ggt gag tca ggg ttc tcc aaa tct atc aca gcc tac gtc tgc	1494			
165	Pro Glu Gly Glu Ser Gly Phe Ser Lys Ser Ile Thr Ala Tyr Val Cys				
166	475	480	485		
168	cag gca gtc atc atc ccc cca gag gtg aca ggc tac aag gcc ggg gtt	1542			
169	Gln Ala Val Ile Ile Pro Glu Val Thr Gly Tyr Lys Ala Gly Val				
170	490	495	500		
172	tcc tca cag cct gtc agc ctt gct gat cga ctt att ggg gtg aca aca	1590			
173	Ser Ser Gln Pro Val Ser Leu Ala Asp Arg Leu Ile Gly Val Thr Thr				
174	505	510	515	520	
176	gat atg act ctg gat gga atc acc tcc cca gct gaa ctt ttc cac ctg	1638			
177	Asp Met Thr Leu Asp Gly Ile Thr Ser Pro Ala Glu Leu Phe His Leu				
178	525	530	535		
180	gag tcc ttg gga ata ccg gac gtg atc ttc ttt tat agg tcc aat gat	1686			
181	Glu Ser Leu Gly Ile Pro Asp Val Ile Phe Phe Tyr Arg Ser Asn Asp				
182	540	545	550		
184	gtg acc cag tcc tgc agt tct ggg aga tca acc acc atc cgc gtc agg	1734			
185	Val Thr Gln Ser Cys Ser Ser Gly Arg Ser Thr Thr Ile Arg Val Arg				
186	555	560	565		
188	tgc agt cca cag aaa act gtc cct gga agt ttg ctg ctg cca gga acg	1782			
189	Cys Ser Pro Gln Lys Thr Val Pro Gly Ser Leu Leu Leu Pro Gly Thr				
190	570	575	580		
192	tgc tca gat ggg acc tgt gat ggc tgc aac ttc cac ttc ctg tgg gag	1830			
193	Cys Ser Asp Gly Thr Cys Asp Gly Cys Asn Phe His Phe Leu Trp Glu				
194	585	590	595	600	

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196 agc gcg gct gct tgc ccg ctc tgc tca gtg gct gac tac cat gct atc 1878
197 Ser Ala Ala Ala Cys Pro Leu Cys Ser Val Ala Asp Tyr His Ala Ile
198 605 610 615
200 gtc agc agc tgt gtg gct ggg atc cag aag act act tac gtg tgg cga 1926
201 Val Ser Ser Cys Val Ala Gly Ile Gln Lys Thr Thr Tyr Val Trp Arg
202 620 625 630
204 gaa ccc aag cta tgc tct ggt ggc att tct ctg cct gag cag aga gtc 1974
205 Glu Pro Lys Leu Cys Ser Gly Gly Ile Ser Leu Pro Glu Gln Arg Val
206 635 640 645
208 acc atc tgc aaa acc ata gat ttc tgg ctg aaa gtg ggc atc tct gca 2022
209 Thr Ile Cys Lys Thr Ile Asp Phe Trp Leu Lys Val Gly Ile Ser Ala
210 650 655 660
212 ggc acc tgt act gcc atc ctg ctc acc gtc ttg acc tgc tac ttt tgg 2070
213 Gly Thr Cys Thr Ala Ile Leu Leu Thr Val Leu Thr Cys Tyr Phe Trp
214 665 670 675 680
216 aaa aag aat caa aaa cta gag tac aag tac tcc aag ctg gtg atg aat 2118
217 Lys Lys Asn Gln Lys Leu Glu Tyr Lys Tyr Ser Lys Leu Val Met Asn
218 685 690 695
220 gct act ctc aag gac tgt gac ctg cca gca gct gac agc tgc gcc atc 2166
221 Ala Thr Leu Lys Asp Cys Asp Leu Pro Ala Ala Asp Ser Cys Ala Ile
222 700 705 710
224 atg gaa ggc gag gat gta gag gac gac ctc atc ttt acc agc aag aat 2214
225 Met Glu Gly Glu Asp Val Glu Asp Asp Leu Ile Phe Thr Ser Lys Asn
226 715 720 725
228 cac tct ttg gga aga tca aat cat tta cct cca aga gga ctc ctg atg 2262
229 His Ser Leu Gly Arg Ser Asn His Leu Pro Pro Arg Gly Leu Leu Met
230 730 735 740
232 gat ttg act cag tgc cgc tga agacatcctc aggaggccca gacatggacc 2313
233 Asp Leu Thr Gln Cys Arg
234 745 750
236 tgtgagaggc actgctgcc tcacctgcct cctcaccttg catagcacct ttgcaagcct 2373
238 gcggcgattt ggggtgccagc atcctgcaac acccactgct ggaaatctct tcattgtggc 2433
240 cttatcagat gtttgaattt cagatctttt tttatagagt acccaaaccc tcctttctgc 2493
242 ttgcctcaaa cctgcctaat ataccacac tttgtttgta aattaaaaaa aaaaaaaaaa 2553
244 a 2554
247 <210> SEQ ID NO: 2
248 <211> LENGTH: 750
249 <212> TYPE: PRT
250 <213> ORGANISM: Homo sapiens
252 <400> SEQUENCE: 2
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254 1 5 10 15
256 Arg Gly Gly Leu His Phe Arg Met Leu Pro Leu Gln Thr Trp His Val
257 20 25 30
259 Cys Arg Gln Ala Gly Leu Leu Phe Leu Gln Thr Leu Pro Ser Asn Ser
260 35 40 45
262 Tyr Ser Asn Lys Gly Glu Thr Ser Cys His Gln Cys Asp Pro Asp Lys
263 50 55 60
265 Tyr Ser Glu Lys Gly Ser Ser Ser Cys Asn Val Arg Pro Ala Cys Thr

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266	65					70						75					80
268	Asp	Lys	Asp	Tyr	Phe	Tyr	Thr	His	Thr	Ala	Cys	Asp	Ala	Asn	Gly	Glu	
269					85					90					95		
271	Thr	Gln	Leu	Met	Tyr	Lys	Trp	Ala	Lys	Pro	Lys	Ile	Cys	Ser	Glu	Asp	
272				100					105					110			
274	Leu	Glu	Gly	Ala	Val	Lys	Leu	Pro	Ala	Ser	Gly	Val	Lys	Thr	His	Cys	
275			115					120					125				
277	Pro	Pro	Cys	Asn	Pro	Gly	Phe	Phe	Lys	Thr	Asn	Asn	Ser	Thr	Cys	Gln	
278		130					135					140					
280	Pro	Cys	Pro	Tyr	Gly	Ser	Tyr	Ser	Asn	Gly	Ser	Asp	Cys	Thr	Arg	Cys	
281	145					150				155						160	
283	Pro	Ala	Gly	Thr	Glu	Pro	Ala	Val	Gly	Phe	Glu	Tyr	Lys	Trp	Trp	Asn	
284				165						170					175		
286	Thr	Leu	Pro	Thr	Asn	Met	Glu	Thr	Thr	Val	Leu	Ser	Gly	Ile	Asn	Phe	
287				180					185					190			
289	Glu	Tyr	Lys	Gly	Met	Thr	Gly	Trp	Glu	Val	Ala	Gly	Asp	His	Ile	Tyr	
290			195					200					205				
292	Thr	Ala	Ala	Gly	Ala	Ser	Asp	Asn	Asp	Phe	Met	Ile	Leu	Thr	Leu	Val	
293		210					215					220					
295	Val	Pro	Gly	Phe	Arg	Pro	Pro	Gln	Ser	Val	Met	Ala	Asp	Thr	Glu	Asn	
296	225					230				235						240	
298	Lys	Glu	Val	Ala	Arg	Ile	Thr	Phe	Val	Phe	Glu	Thr	Leu	Cys	Ser	Val	
299				245						250					255		
301	Asn	Cys	Glu	Leu	Tyr	Phe	Met	Val	Gly	Val	Asn	Ser	Arg	Thr	Asn	Thr	
302				260					265					270			
304	Pro	Val	Glu	Thr	Trp	Lys	Gly	Ser	Lys	Gly	Lys	Gln	Ser	Tyr	Thr	Tyr	
305		275						280					285				
307	Ile	Ile	Glu	Glu	Asn	Thr	Thr	Thr	Ser	Phe	Thr	Trp	Ala	Phe	Gln	Arg	
308		290					295					300					
310	Thr	Thr	Phe	His	Glu	Ala	Ser	Arg	Lys	Tyr	Thr	Asn	Asp	Val	Ala	Lys	
311	305				310						315					320	
313	Ile	Tyr	Ser	Ile	Asn	Val	Thr	Asn	Val	Met	Asn	Gly	Val	Ala	Ser	Tyr	
314				325						330					335		
316	Cys	Arg	Pro	Cys	Ala	Leu	Glu	Ala	Ser	Asp	Val	Gly	Ser	Ser	Cys	Thr	
317				340					345					350			
319	Ser	Cys	Pro	Ala	Gly	Tyr	Tyr	Ile	Asp	Arg	Asp	Ser	Gly	Thr	Cys	His	
320			355					360					365				
322	Ser	Cys	Pro	Pro	Asn	Thr	Ile	Leu	Lys	Ala	His	Gln	Pro	Tyr	Gly	Val	
323		370					375					380					
325	Gln	Ala	Cys	Val	Pro	Cys	Gly	Pro	Gly	Thr	Lys	Asn	Asn	Lys	Ile	His	
326	385					390					395					400	
328	Ser	Leu	Cys	Tyr	Asn	Asp	Cys	Thr	Phe	Ser	Arg	Asn	Thr	Pro	Thr	Arg	
329				405						410					415		
331	Thr	Phe	Asn	Tyr	Asn	Phe	Ser	Ala	Leu	Ala	Asn	Thr	Val	Thr	Leu	Ala	
332				420					425					430			
334	Gly	Gly	Pro	Ser	Phe	Thr	Ser	Lys	Gly	Leu	Lys	Tyr	Phe	His	His	Phe	
335			435					440					445				
337	Thr	Leu	Ser	Leu	Cys	Gly	Asn	Gln	Gly	Arg	Lys	Met	Ser	Val	Cys	Thr	
338		450					455					460					

Use of Xaa or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:621 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:867 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:873 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:875 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:899 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:923 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:927 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:929 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:952 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:956 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1014 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1020 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1022 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1040 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1415 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1421 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1437 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1528 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1532 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1536 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1595 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1597 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:2410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48

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L:2412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:2436 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:2452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50